Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	122540	(synthetic or variant or modif$ or alter$) near5 (gene$1 or sequence$1 or nucleic acid$1)	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:44
L2	4828	codon near3 (choice$1 or preference$1 or select$)	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:45
L3	2438	1 same 2	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:46
L4	54714	(transcription factor$1 or splice or promoter$1 or polyadenylat$) near5 (site$1 or sequence$1)	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:46
L5	16128	1 same 4	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:46
L6	1411	3 and 5	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:47
L7	152	1 same 2 same 4	US-PGPUB; USPAT	ADJ	OFF	2005/03/07 11:47

8/24/00

PGPUB-DOCUMENT-NUMBER: 20050050586

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050050586 A1

TITLE: AP1 amine oxidase variants

PUBLICATION-DATE: March 3, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Chatterjee, Ranjini	Belmont	CA	US	
Duvick, Jonathan P.	Des Moines	IA	US	
English, James	San Leandro	CA	US	

APPL-NO: 10/ 872750

DATE FILED: June 21, 2004

RELATED-US-APPL-DATA:

child 10872750 A1 20040621

parent continuation-of 10636974 20030806 US PENDING

child 10872750 A1 20040621

parent continuation-in-part-of 10072307 20020206 US ABANDONED

non-provisional-of-provisional 60478188 20030613 US

non-provisional-of-provisional 60401629 20020806 US

non-provisional-of-provisional 60266918 20010206 US

non-provisional-of-provisional 60300324 20010622 US

US-CL-CURRENT: 800/279, 435/197 , 435/419 , 435/468 , 435/69.1 , 536/23.2

ABSTRACT:

New fumonisin detoxifying or fumonisin-derivative detoxifying homologues (both nucleic acids and proteins) are provided. Compositions which include these new proteins, recombinant cells, antibodies to the new homologues, and methods of using the homologues are also provided.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Ser. No. 10/636,974, filed Aug. 6, 2003, which claims priority to and benefit of U.S. Provisional Patent Application Ser. No. 60/401,629, filed on Aug. 6, 2002, the disclosures of which are incorporated herein by reference in their entirety for all purposes and U.S. Provisional Patent Application Ser. No. 60/478,188, filed on Jun. 13, 2003, the disclosure of which is incorporated herein in its entirety for all purposes; and this application is a continuation-in-part of and claims priority to and benefit of co-pending U.S. application Ser. No. 10/072,307 filed on Feb. 6, 2002 the disclosure of which is incorporated

herein by reference in its entirety for all purposes, which claims priority to and benefit of U.S. Provisional Patent Application Ser. No. 60/266,918 filed on Feb. 6, 2001, the disclosure of which is incorporated herein by reference in its entirety for all purposes and U.S. Provisional Patent Application Ser. No. 60/300,324, filed on Jun. 22, 2001, the disclosure of which is incorporated herein in its entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (56):

[0106] The polynucleotide sequences of the present invention can be engineered in order to alter the FD/FDD homologue coding sequence of the invention for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, alterations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to introduce splice sites, etc. Further details regarding silent and conservative substitutions are provided below.

PGPUB-DOCUMENT-NUMBER: 20050037021

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050037021 A1

TITLE: Baculovirus produced Plasmodium falciparum vaccine

PUBLICATION-DATE: February 17, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Chang, Sandra P.	Honolulu	HI	US	
Hashimoto, Ann	Kaneohe	HI	US	
Nishimura, Tani	Honolulu	HI	US	

APPL-NO: 10/ 935793

DATE FILED: September 7, 2004

RELATED-US-APPL-DATA:

child 10935793 A1 20040907

parent division-of 10062809 20020201 US ABANDONED

US-CL-CURRENT: 424/191.1, 435/348 , 435/456 , 435/69.3 , 530/350 , 536/23.5

ABSTRACT:

Compositions and methods are provided for the induction of a protective immunize response in primates against a lethal challenge of Plasmodium.

[0001] This application is a continuation-in-part of application Ser. No. 09/500,376, filed Feb. 8, 2000, now pending and claims priority to provisional Application No. 60/266,281, filed Feb. 1, 2001.

---------- KWIC ---------

Detail Description Paragraph - DETX (163):

[0202] The K1 type (p42-K) of the p42 antigen was constructed using the Vietnam-Oak Knoll P. falciparum isolate (FVO). There are three parts to this construct: a leader sequence, the p42-K coding region and the histidine tag (FIG. 13). Restriction sites were incorporated into the primers to enable a "sticky-end" ligation of the three fragments. The leader sequence was altered from the original p42-M sequence such that three adenines were added three bases prior to the start site to optimize the codon preference for baculovirus and insect cells as well as the distance between the promoter sequence and the methionine start codon (Ranjan et al. 1995. Virus Genes 9(2):149-153). Primers containing NarI and PstI restriction site sequences were used to amplify the 1,065 base pair p42-K coding region corresponding to the Ala.sub.1349 to Ser.sub.1723 (as numbered by Miller et al. 1993. Mol. Biochem. Parasitol 59(1):1-14.) of MSP-1 from genomic P. falciparum DNA. Primers containing BamHI and NarI restriction site sequences were used to amplify the 91 base pair leader sequence. Oligonucleotides containing PstI and KpnI

restriction site sequences were made to generate the 25 base pair histidine tag. All primers and oligonucleotide sequences used for the p42-K constructs are shown in Table 1.

PGPUB-DOCUMENT-NUMBER: 20050032083

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050032083 A1

TITLE: Nucleic acid encoding spinocerebellar ataxia-2 and products related thereto

PUBLICATION-DATE: February 10, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Pulst, Stefan M.	Los Angeles	CA	US	

APPL-NO: 10/ 750323

DATE FILED: December 30, 2003

RELATED-US-APPL-DATA:

child 10750323 A1 20031230

parent continuation-of 09083268 19980522 US GRANTED

parent-patent 6673535 US

child 09083268 19980522 US

parent division-of 08727084 19961008 US ABANDONED

non-provisional-of-provisional 60022207 19960719 US

non-provisional-of-provisional 60017388 19960508 US

US-CL-CURRENT: 435/6, 435/320.1 , 435/325 , 435/69.1 , 530/350 , 536/23.5

ABSTRACT:

The present invention provides isolated nucleic acids encoding human SCA2 protein, or fragments thereof, and isolated SCA2 proteins encoded thereby. Further provided are vectors containing invention nucleic acids, probes that hybridize thereto, host cells transformed therewith, antisense oligonucleotides thereto and compositions containing antibodies that specifically bind to invention polypeptides, as well as transgenic non-human mammals that express the invention protein. In addition, methods for diagnosing spinocerebellar Ataxia Type 2 are provided.

RELATED THERETO

[0001] This application is a continuation application of U.S. application Ser. No. 09/083,268, filed May 22, 1998, which is a divisional of U.S. patent application Ser. No. 08/727,084, filed Oct. 8, 1996, now abandoned, which claims the benefit of U.S. Provisional Application No. 60/017,388, filed May 8, 1996, now abandoned, and U.S. Provisional Application No. 60/022,207, filed Jul. 19, 1996, now abandoned. The entire teachings of the above applications are incorporated herein by reference.

---------- KWIC ---------

Detail Description Paragraph - DETX (23):

[0043] Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA in vitro or in vivo, and are commercially available from sources such as Stratagene (La Jolla, Calif.) and Promega Biotech (Madison, Wis.). In order to optimize expression and/or in vitro transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the clones to eliminate extra, potential inappropriate alternative translation initiation codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5' of the start codon to enhance expression. (See, for example, Kozak, J. Biol. Chem. 266:19867 (1991)). Similarly, alternative codons, encoding the same amino acid, can be substituted for coding sequences of the SCA2 polypeptide in order to enhance transcription (e.g., the codon preference of the host cell can be adopted, the presence of G-C rich domains can be reduced, and the like).

PGPUB-DOCUMENT-NUMBER: 20050025742

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050025742 A1

TITLE: Methods and compositions for interferon therapy

PUBLICATION-DATE: February 3, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Engler, Heidrun	San Diego	CA	US	
Nagabhushan, Tattanahalli L.	Parsippany	NJ	US	
Youngster, Stephen	Piscataway	NJ	US	
Connor, Robert	Oceanside	CA	US	

APPL-NO: 10/ 861654

DATE FILED: June 4, 2004

RELATED-US-APPL-DATA:

child 10861654 A1 20040604

parent continuation-in-part-of 10455215 20030604 US PENDING

child 10455215 20030604 US

parent continuation-in-part-of 10055863 20020122 US PENDING

child 10055863 20020122 US

parent continuation-of 09112074 19980708 US GRANTED

parent-patent 6392069 US

child 09112074 19980708 US

parent continuation-in-part-of 08889355 19970708 US PENDING

child 08889355 19970708 US

parent continuation-in-part-of 08584077 19960108 US GRANTED

parent-patent 5789244 US

child 10861654 A1 20040604

parent continuation-in-part-of 10454662 20030603 US PENDING

child 10454662 20030603 US

parent continuation-of 09650359 20000828 US ABANDONED

child 09650359 20000828 US

parent continuation-of 08779627 19970107 US GRANTED

parent-patent 6165779 US

child 08779627 19970107 US

parent continuation-in-part-of 08584077 19960108 US GRANTED

parent-patent 5789244 US

non-provisional-of-provisional 60475926 20030604 US

US-CL-CURRENT: 424/85.4, 424/85.7 , 514/44

ABSTRACT:

Methods and pharmaceutical compositions for administering protein or gene therapy to tissues or organs having an epithelial cell layer are provided. A protein or nucleic acid encoding the protein is administered to the target tissue or organ in combination with treatment with a delivery enhancing agent which increases the delivery of the interferon or nucleic acid to the cells of the target tissues or organs. The methods and combinations are particularly useful in the treatment of cancers and other conditions responsive to interferon therapy. An exemplary method comprises the transurethral intravesical administration to the bladder of a therapeutically effective amount of a pharmaceutical composition comprising an alpha-interferon or a gene delivery system encoding the interferon and SYN3 or a SYN3 homolog or analog. In the urinary bladder, as much as a 10 to 1000 fold increased in interferon levels and activity may be observed with the use of a SYN3 formulation as opposed to a PBS formulation of the same interferon protein or interferon gene delivery system.

CROSS-REFERENCES TO RELATED APPLICATIONS

[0001] This application is a continuation-in-part of U.S. patent application Ser. No. 10/455,215 filed Jun. 4, 2003 which is a continuation-in-part of U.S. patent application Ser. No. 10/055,863, filed Jan. 22, 2002, which is a continuation of U.S. patent application Ser. No. 09/112,074, filed on Jul. 8, 1998 (U.S. Pat. No. 6,392,069, issued on May 21, 2002), which is a continuation in part of U.S. patent application Ser. No. 08/889,355, filed on Jul. 8, 1997, which is a continuation in part of U.S. patent application Ser. No. 08/584,077, filed Jan. 8, 1996 (U.S. Pat. No. 5,789,244, issued on Aug. 4, 1998); this application is also a continuation in part of U.S. patent application Ser. No. to be assigned, filed on Jun. 3, 2003, (Townsend and Townsend and Crew LLP Attorney Docket No. 016930-000815), which is a continuation of U.S. patent application Ser. No. 09/650,359, filed on Aug. 28, 2000, which is a continuation of U.S. patent application Ser. No. 08/779,627, filed Jan. 7, 1997 (U.S. Pat. No. 6,165,779, issued on Dec. 26, 2000), which is a continuation in part of U.S. patent application Ser. No. 08/584,077, filed on Jan. 8, 1996; this application claims priority to U.S. patent application Ser. No. to be assigned, filed on Jun. 4, 2004, (Townsend and Townsend and Crew LLP Attorney Docket No. 016930-000831US which claims the benefit of U.S. patent application No. 60/475926 filed on Jun. 4, 2003. This application contains subject matter related to that of U.S. patent application Ser. No. 10/329,043, filed on Dec. 20, 2002 which claims the benefit of U.S. patent application Ser. No. 60/342329 filed on Dec. 20, 2001. The disclosures of these priority applications are herein incorporated by reference in their entireties for all purposes.

---------- KWIC --------

Detail Description Paragraph - DETX (14):

[0037] The term "gene" as used herein is intended to refer to a nucleic acid sequence which encodes an polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term "gene" may include not only coding sequences but also regulatory regions such as promoters, enhancers, and termination regions. The term further can include all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites. Nucleic acid sequences encoding the polypeptide can be DNA or RNA which directs the expression of a specific protein or peptide. These nucleic acid sequences may be a DNA strand sequence that is transcribed into RNA or an RNA sequence that is translated into protein. The nucleic acid sequences include both the full-length nucleic acid sequences as well as non-full length sequences derived from the full-length protein. It is further understood that the sequence includes the degenerate codons of the native sequence or sequences that may be introduced to provide codon preference in a specific host cell.

PGPUB-DOCUMENT-NUMBER: 20050013825

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20050013825 A1

TITLE: Vaccine containing the catalytic subunit of telomerase for treating cancer

PUBLICATION-DATE: January 20, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Cech, Thomas R.	Potomac	MD	US	
Lingner, Joachim	Epalinges	CA	CH	
Nakamura, Toru	San Diego	MA	US	
Chapman, Karen B.	Southborough	CA	US	
Morin, Gregg B.	Oakville	NV	CA	
Harley, Calvin B.	Palo Alto		US	
Andrews, William H.	Reno		US	

APPL-NO: 10/ 877146

DATE FILED: June 24, 2004

RELATED-US-APPL-DATA:

child 10877146 A1 20040624

parent continuation-in-part-of 09843676 20010426 US PENDING

child 10877146 A1 20040624

parent continuation-in-part-of 10044692 20020111 US PENDING

child 10877146 A1 20040624

parent continuation-of 09432503 19991102 US PENDING

child 09432503 19991102 US

parent continuation-of 08974549 19971119 US GRANTED

parent-patent 6166178 US

child 08974549 19971119 US

parent continuation-in-part-of 08915503 19970814 US ABANDONED

child 08974549 19971119 US

parent continuation-in-part-of 08912951 19970814 US GRANTED

parent-patent 6475789 US

child 08974549 19971119 US

parent continuation-in-part-of 08911312 19970814 US ABANDONED

child 08915503

parent continuation-in-part-of 08854050 19970509 US GRANTED

parent-patent 6261836 US

child 08912951

parent continuation-in-part-of 08854050 19970509 US GRANTED

parent-patent 6261836 US

child 08911312

parent continuation-in-part-of 08854050 19970509 US GRANTED

parent-patent 6261836 US

child 08854050 19970509 US

parent continuation-in-part-of 08851843 19970506 US GRANTED

parent-patent 6093809 US

child 08851843 19970506 US

parent continuation-in-part-of 08846017 19970425 US ABANDONED

child 08846017 19970425 US

parent continuation-in-part-of 08844419 19970418 US ABANDONED

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US97/17885	1997WO-PCT/US97/17885	October 1, 1997
WO	PCT/US97/17618	1997WO-PCT/US97/17618	October 1, 1997

US-CL-CURRENT: 424/185.1, 435/183 , 435/320.1 , 435/325 , 435/69.1 , 530/350 , 536/23.5

ABSTRACT:

The invention provides compositions and methods related to human telomerase reverse transcriptase (hTRT), the catalytic protein subunit of human telomerase. The polynucleotides and polypeptides of the invention are useful for diagnosis, prognosis and treatment of human diseases, for changing the proliferative capacity of cells and organisms, and for identification and screening of compounds and treatments useful for treatment of diseases such as cancers.

[0001] This application is a continuation-in-part of U.S. application Ser. No. 09/843,676, filed Apr. 26, 2001, and a continuation-in part of U.S. application Ser. No. 10/044,692, filed Jan. 11, 2002, and a continuation of U.S. patent application Ser. No. 09/432,503, filed Nov. 2, 1999, which is a continuation of U.S. patent application Ser. No. 08/974,549 filed Nov. 19, 1997, U.S. Pat. No. 6,166,178, which is a continuation-in-part application of

U.S. patent application Ser. No. 08/915,503, filed Aug. 14, 1997, abandoned, and a continuation-in-part application of U.S. patent application Ser. No. 08/912,951, filed Aug. 14, 1997, U.S. Pat. No. 6,475,789 and a continuation-in-part of application of U.S. patent application Ser. No. 08/911,312, filed Aug. 14, 1997, abandoned, all three of which are continuations-in-part of U.S. patent application Ser. No. 08/854,050, filed May 9, 1997, U.S. Pat. No. 6,261,836, which is a continuation-in-part of U.S. patent application Ser. No. 08/851,843, filed May 6, 1997, U.S. Pat. No. 6,093,809, which is a continuation-in-part of U.S. patent application Ser. No. 08/846,017, filed Apr. 25, 1997, abandoned, which is a continuation-in-part of U.S. application Ser. No. 08/844,419 filed Apr. 18, 1997, abandoned. This application also claims priority to Patent Convention Treaty Patent Application Serial No.: PCT/US97/17885 (published on Apr. 9, 1998 as WO 98/14593) and to Patent Convention Treaty Patent Application Serial No.: PCT/US97/17618 (published on Apr. 9, 1998 as WO 98/14592), both designating the U.S. and filed in the U.S. Receiving Office on Oct. 1, 1997. Each of the aforementioned applications is explicitly incorporated herein by reference in its entirety and for all purposes. This application also incorporates by reference copending U.S. patent application Ser. No. 08/974,584, filed Nov. 19, 1997, in its entirety and for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (68):

[0184] The present invention further provides altered or modified hTRT nucleic acids. It will be recognized by one of skill that the cloned or amplified hTRT nucleic acids obtained can be modified (e.g., truncated, derivatized, altered) by methods well known in the art (e.g., site-directed mutagenesis, linker scanning mutagenesis) or simply synthesized de novo as described below. The altered or modified hTRT nucleic acids are useful for a variety of applications, including, but not limited to, facilitating cloning or manipulation of an hTRT gene or gene product, or expressing a variant hTRT gene product. For example, in one embodiment, the hTRT gene sequence is altered such that it encodes an hTRT polypeptide with altered properties or activities, as discussed in detail in infra, for example, by mutation in a conserved motif of hTRT. In another illustrative example, the mutations in the protein coding region of an hTRT nucleic acid may be introduced to alter glycosylation patterns, to change codon preference, to produce splice variants, remove protease-sensitive sites, create antigenic domains, modify specific activity, and the like. In other embodiments, the nucleotide sequence encoding hTRT and its derivatives is changed without altering the encoded amino acid sequences, for example, the production of RNA transcripts having more desirable properties, such as increased translation efficiency or a greater or a shorter half-life, compared to transcripts produced from the naturally occurring sequence. In yet another embodiment, altered codons are selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic expression host in accordance with the frequency with which particular codons are utilized by the host. Useful in vitro and in vivo recombinant techniques that can be used to prepare variant hTRT polynucleotides of the invention are found in Sambrook et al. and Ausubel et al., both supra.

PGPUB-DOCUMENT-NUMBER: 20040265965

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040265965 A1

TITLE: Glycosylation variants of BACE

PUBLICATION-DATE: December 30, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Anderson, John	San Francisco	CA	US	
McConlogue, Lisa	Burlingame	CA	US	
Basi, Guriqbal	Palo Alto	CA	US	
Sinha, Sukanto	San Francisco	CA	US	

APPL-NO: 10/ 837021

DATE FILED: April 30, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60467509 20030502 US

US-CL-CURRENT: 435/69.1, 435/184 , 435/320.1 , 435/325 , 536/23.2

ABSTRACT:

Human BACE polypeptides having modifications to the N-linked glycosylation sites including one or more of the following amino acid substitutions: S174I, N233A, N153Q and N354S. DNA sequences, vectors, and host cells for producing the polypeptides. Crystalline protein compositions formed from the purified polypeptides. Methods of screening for compounds that inhibit A.beta. using the polypeptides.

CROSS REFERNCE TO RELATED APPLICATION

[0001] This application claims the benefit of U.S. Provisional Patent Application Ser. No. 60/467,509 filed May 2, 2003.

---------- KWIC ---------

Detail Description Paragraph - DETX (97):

[0115] The polynucleotide sequences of the present invention can be engineered in order to alter a .beta.-secretase coding sequence for a variety of reasons, including but not limited to, alterations that modify the cloning, processing and/or expression of the gene product. For example, alterations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to change codon preference, to produce splice variants, etc. For example, it may be advantageous to produce .beta.-secretase-encoding nucleotide sequences possessing non-naturally occurring codons. Codons preferred by a particular prokaryotic or eukaryotic host (Murray, E. et al., (1989) Nuc. Acids Res. 17:477-508) can be selected, for example, to increase the rate of .beta.-secretase polypeptide expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than

transcripts produced from naturally occurring sequence. This may be particularly useful in producing recombinant enzyme in non-mammalian cells, such as bacterial, yeast, or insect cells. The present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. Appropriate cloning and expression vectors for use with prokaryotic and eukaryotic hosts are also described in Sambrook, et al., (supra).

PGPUB-DOCUMENT-NUMBER: 20040247613

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040247613 A1

TITLE: Treating cancer using a telomerase vaccine

PUBLICATION-DATE: December 9, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Cech, Thomas R.	Potomac	MD	US	
Lingner, Joachim	Epalinges	CA	CH	
Nakamura, Toru	San Diego	MA	US	
Chapman, Karen B.	Southborough	NV	US	
Morin, Gregg B.	Oakville	CA		
Harley, Calvin B.	Palo Alto	CA		
Andrews, William H.	Reno		US	

APPL-NO: 10/ 877022

DATE FILED: June 24, 2004

RELATED-US-APPL-DATA:

child 10877022 A1 20040624

parent continuation-in-part-of 09843676 20010426 US PENDING

child 10877022 A1 20040624

parent continuation-in-part-of 10044692 20020111 US PENDING

child 10877022 A1 20040624

parent continuation-of 09432503 19991102 US PENDING

child 09432503 19991102 US

parent continuation-of 08974549 19971119 US GRANTED

parent-patent 6166178 US

child 08974549 19971119 US

parent continuation-in-part-of 08915503 19970814 US ABANDONED

child 08974549 19971119 US

parent continuation-in-part-of 08912951 19970814 US GRANTED

parent-patent 6475789 US

child 08974549 19971119 US

parent continuation-in-part-of 08911312 19970814 US ABANDONED

child 08911312 19970814 US

parent continuation-in-part-of 08854050 19970509 US GRANTED

parent-patent 6261836 US

child 08854050 19970509 US

parent continuation-in-part-of 08851843 19970506 US GRANTED

parent-patent 6093809 US

child 08851843 19970506 US

parent continuation-in-part-of 08846017 19970425 US ABANDONED

child 08846017 19970425 US

parent continuation-in-part-of 08844419 19970418 US ABANDONED

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US97/17885	1997WO-PCT/US97/17885	October 1, 1997
WO	PCT/US97/17618	1997WO-PCT/US97/17618	October 1, 1997

US-CL-CURRENT: 424/185.1

ABSTRACT:

The invention provides compositions and methods related to human telomerase reverse transcriptase (hTRT), the catalytic protein subunit of human telomerase. The polynucleotides and polypeptides of the invention are useful for diagnosis, prognosis and treatment of human diseases, for changing the proliferative capacity of cells and organisms, and for identification and screening of compounds and treatments useful for treatment of diseases such as cancers.

[0001] This application is a continuation-in-part of U.S. application Ser. No. 09/843,676, filed Apr. 26, 2001, and a continuation-in part of U.S. application Ser. No. 10/044,692, filed Jan. 11, 2002, and a continuation of U.S. patent application Ser. No. 09/432,503, filed Nov. 2, 1999, which is a continuation of U.S. patent application Ser. No. 08/974,549 filed Nov. 19, 1997, U.S. Pat. No. 6,166,178, which is a continuation-in-part application of U.S. patent application Ser. No. 08/915,503, filed Aug. 14, 1997, abandoned, and a continuation-in-part application of U.S. patent application Ser. No. 08/912,951, filed Aug. 14, 1997, U.S. Pat. No. 6,475,789 and a continuation-in-part of application of U.S. patent application Ser. No. 08/911,312, filed Aug. 14, 1997, abandoned, all three of which are continuations-in-part of U.S. patent application Ser. No. 08/854,050, filed May 9, 1997, U.S. Pat. No. 6,261,836, which is a continuation-in-part of U.S. patent application Ser. No. 08/851,843, filed May 6, 1997, U.S. Pat. No. 6,093,809, which is a continuation-in-part of U.S. patent application Ser. No. 08/846,017, filed Apr. 25, 1997, abandoned, which is a continuation-in-part of U.S. application Ser. No. 08/844,419 filed Apr. 18, 1997, abandoned. This application also claims priority to Patent Convention Treaty Patent Application Serial No.: PCT/US97/17885 (published on Apr. 9, 1998 as WO 98/14593) and to Patent Convention Treaty Patent Application Serial

No.: PCT/US97/17618 (published on Apr. 9, 1998 as WO 98/14592), both designating the U.S. and filed in the U.S. Receiving Office on Oct. 1, 1997. Each of the aforementioned applications is explicitly incorporated herein by reference in its entirety and for all purposes. This application also incorporates by reference copending U.S. patent application Ser. No. 08/974,584, filed Nov. 19, 1997, in its entirety and for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (61):

[0177] The present invention further provides altered or modified hTRT nucleic acids. It will be recognized by one of skill that the cloned or amplified hTRT nucleic acids obtained can be modified (e.g., truncated, derivatized, altered) by methods well known in the art (e.g., site-directed mutagenesis, linker scanning mutagenesis) or simply synthesized de novo as described below. The altered or modified hTRT nucleic acids are useful for a variety of applications, including, but not limited to, facilitating cloning or manipulation of an hTRT gene or gene product, or expressing a variant hTRT gene product. For example, in one embodiment, the hTRT gene sequence is altered such that it encodes an hTRT polypeptide with altered properties or activities, as discussed in detail in infra, for example, by mutation in a conserved motif of hTRT. In another illustrative example, the mutations in the protein coding region of an hTRT nucleic acid may be introduced to alter glycosylation patterns, to change codon preference, to produce splice variants, remove protease-sensitive sites, create antigenic domains, modify specific activity, and the like. In other embodiments, the nucleotide sequence encoding hTRT and its derivatives is changed without altering the encoded amino acid sequences, for example, the production of RNA transcripts having more desirable properties, such as increased translation efficiency or a greater or a shorter half-life, compared to transcripts produced from the naturally occurring sequence. In yet another embodiment, altered codons are selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic expression host in accordance with the frequency with which particular codons are utilized by the host. Useful in vitro and in vivo recombinant techniques that can be used to prepare variant hTRT polynucleotides of the invention are found in Sambrook et al. and Ausubel et al., both supra.

PGPUB-DOCUMENT-NUMBER: 20040242529

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040242529 A1

TITLE: Vector encoding inactivated telomerase for treating cancer

PUBLICATION-DATE: December 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Cech, Thomas R.	Potomac	MD	US	
Lingner, Joachim	Epalingers	CA	CH	
Nakamura, Toru	San Diego	MA	US	
Chapman, Karen B.	Southborough	CA	US	
Morin, Gregg B.	Oakville	NV	CA	
Harley, Calvin B.	Palo Alto		US	
Andrews, William H.	Reno		US	

APPL-NO: 10/ 877124

DATE FILED: June 24, 2004

RELATED-US-APPL-DATA:

child 10877124 A1 20040624

parent continuation-in-part-of 09843676 20010426 US PENDING

child 10877124 A1 20040624

parent continuation-in-part-of 10044692 20020111 US PENDING

child 10877124 A1 20040624

parent continuation-in-part-of 09432503 19991102 US PENDING

child 09432503 19991102 US

parent continuation-of 08974549 19971119 US GRANTED

parent-patent 6166178 US

child 08974549 19971119 US

parent continuation-in-part-of 08915503 19970814 US ABANDONED

child 08974549 19971119 US

parent continuation-in-part-of 08912951 19970814 US GRANTED

parent-patent 6475789 US

child 08974549 19971119 US

parent continuation-in-part-of 08911312 19970814 US ABANDONED

child 08911312 19970814 US

parent continuation-in-part-of 08854050 19970509 US GRANTED

parent-patent 6261836 US

child 08854050 19970509 US

parent continuation-in-part-of 08851843 19970506 US GRANTED

parent-patent 6093809 US

child 08851843 19970506 US

parent continuation-in-part-of 08846017 19970425 US ABANDONED

child 08846017 19970425 US

parent continuation-in-part-of 08844419 19970418 US ABANDONED

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
WO	PCT/US97/17885	1997WO-PCT/US97/17885	October 1, 1997
WO	PCT/US97/17618	1997WO-PCT/US97/17618	October 1, 1997

US-CL-CURRENT: 514/44, 435/320.1 , 435/455

ABSTRACT:

The invention provides compositions and methods related to human telomerase reverse transcriptase (hTRT), the catalytic protein subunit of human telomerase. The polynucleotides and polypeptides of the invention are useful for diagnosis, prognosis and treatment of human diseases, for changing the proliferative capacity of cells and organisms, and for identification and screening of compounds and treatments useful for treatment of diseases such as cancers.

[0001] This application is a continuation-in-part of U.S. application Ser. No. 09/843,676, filed Apr. 26, 2001, and a continuation-in part of U.S. application Ser. No. 10/044,692, filed Jan. 11, 2002, and a continuation of U.S. patent application Ser. No. 09/432,503, filed Nov. 2, 1999, which is a continuation of U.S. patent application Ser. No. 08/974,549 filed Nov. 19, 1997, U.S. Pat. No. 6,166,178, which is a continuation-in-part application of U.S. patent application Ser. No. 08/915,503, filed Aug. 14, 1997, abandoned, and a continuation-in-part application of U.S. patent application Ser. No. 08/912,951, filed Aug. 14, 1997, U.S. Pat. No. 6,475,789 and a continuation-in-part of application of U.S. patent application Ser. No. 08/911,312, filed Aug. 14, 1997, abandoned, all three of which are continuations-in-part of U.S. patent application Ser. No. 08/854,050, filed May 9, 1997, U.S. Pat. No. 6,261,836, which is a continuation-in-part of U.S. patent application Ser. No. 08/851,843, filed May 6, 1997, U.S. Pat. No. 6,093,809, which is a continuation-in-part of U.S. patent application Ser. No. 08/846,017, filed Apr. 25, 1997, abandoned, which is a continuation-in-part of U.S. application Ser. No. 08/844,419 filed Apr. 18, 1997, abandoned. This application also claims priority to Patent Convention Treaty Patent Application Serial No.: PCT/US97/17885 (published on Apr. 9,

1998 as WO 98/14593) and to Patent Convention Treaty Patent Application Serial No.: PCT/US97/17618 (published on Apr. 9, 1998 as WO 98/14592), both designating the U.S. and filed in the U.S. Receiving Office on Oct. 1, 1997. Each of the aforementioned applications is explicitly incorporated herein by reference in its entirety and for all purposes. This application also incorporates by reference copending U.S. patent application Ser. No. 08/974,584, filed Nov. 19, 1997, in its entirety and for all purposes.

---------- KWIC --------

Detail Description Paragraph - DETX (61):

[0176] The present invention further provides altered or modified hTRT nucleic acids. It will be recognized by one of skill that the cloned or amplified hTRT nucleic acids obtained can be modified (e.g., truncated, derivatized, altered) by methods well known in the art (e.g., site-directed mutagenesis, linker scanning mutagenesis) or simply synthesized de novo as described below. The altered or modified hTRT nucleic acids are useful for a variety of applications, including, but not limited to, facilitating cloning or manipulation of an hTRT gene or gene product, or expressing a variant hTRT gene product. For example, in one embodiment, the hTRT gene sequence is altered such that it encodes an hTRT polypeptide with altered properties or activities, as discussed in detail in infra, for example, by mutation in a conserved motif of hTRT. In another illustrative example, the mutations in the protein coding region of an hTRT nucleic acid may be introduced to alter glycosylation patterns, to change codon preference, to produce splice variants, remove protease-sensitive sites, create antigenic domains, modify specific activity, and the like. In other embodiments, the nucleotide sequence encoding hTRT and its derivatives is changed without altering the encoded amino acid sequences, for example, the production of RNA transcripts having more desirable properties, such as increased translation efficiency or a greater or a shorter half-life, compared to transcripts produced from the naturally occurring sequence. In yet another embodiment, altered codons are selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic expression host in accordance with the frequency with which particular codons are utilized by the host. Useful in vitro and in vivo recombinant techniques that can be used to prepare variant hTRT polynucleotides of the invention are found in Sambrook et al. and Ausubel et al., both supra.

PGPUB-DOCUMENT-NUMBER: 20040241650

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040241650 A1

TITLE: Computer-directed assembly of a polynucleotide encoding a target polypeptide

PUBLICATION-DATE: December 2, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Evans, Glen A	San Marcos	CA	US	

APPL-NO: 10/ 250894

DATE FILED: December 30, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60262693 20010119 US

PCT-DATA:
APPL-NO: PCT/US02/01649
DATE-FILED: Jan 18, 2002
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 435/6, 435/91.2

ABSTRACT:

The present invention outlines a novel approach to utilizing the results of genomic sequence information by computer-directed polynucleotide assembly based upon information available in databases such as the human genome database. Specifically, the present invention may be used to select, synthesize and assemble a novel, synthetic target polynucleotide sequence encoding a target polypeptide. The target polynucleotide may encode a target polypeptide that exhibits enhanced or altered biological activity as compared to a model polypeptide encoded by a natural (wild-type) or model polynucleotide sequence.

---------- KWIC ---------

Detail Description Paragraph - DETX (161):
[0195] In addition to the above codon preferences, specific promoter, enhancer, replication or drug resistance sequences can be included in a synthetic nucleic acid sequence of the invention. The length of the construction can be adjusted by padding to give a round number of bases based on about 25 to 100 bp synthesis. The synthesis of sequences of about 25 to 100 bp in length can be manufactured and assembled using the array synthesizer system and may be used without further purification. For example, two 96-well plates containing 100-mers could give a 9600 bp construction of a target sequence.

PGPUB-DOCUMENT-NUMBER: 20040219131

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040219131 A1

TITLE: Interferon-alpha polypeptides and conjugates

PUBLICATION-DATE: November 4, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Patten, Phillip A.	Portola Valley	CA	US	
Govindarajan, Sridhar	Redwood City	CA	US	
Viswanathan, Sridhar	Menlo Park	CA	US	
Nissen, Torben Lauesgaard	San Francisco	CA	US	

APPL-NO: 10/ 714817

DATE FILED: November 17, 2003

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60502560 20030912 US

non-provisional-of-provisional 60427612 20021118 US

US-CL-CURRENT: 424/85.7, 435/320.1 , 435/325 , 435/69.51 , 530/351 , 536/23.5

ABSTRACT:

The present invention provides interferon-alpha polypeptides and conjugates, and nucleic acids encoding the polypeptides. The invention also includes compositions comprising these polypeptides, conjugates, and nucleic acids; cells containing or expressing the polypeptides, conjugates, and nucleic acids; methods of making the polypeptides, conjugates, and nucleic acids; and methods of using the polypeptides, conjugates, and nucleic acids.

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] Pursuant to 35 U.S.C. .sctn. 119(e), this application claims the benefit of U.S. Provisional Application Ser. No. 60/502,560 filed on Sep. 12, 2003 and U.S. Provisional Application Ser. No. 60/427,612 filed on Nov. 18, 2002, the disclosures of each of which are incorporated by reference herein in their entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (260):

[0291] The polynucleotide sequences of the present invention can be engineered in order to alter a coding sequence of the invention for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, alterations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns, to introduce or remove attachment groups (e.g., for

pegylation or other conjugation), to change codon preference, to introduce splice sites, etc.

PGPUB-DOCUMENT-NUMBER: 20040203130

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040203130 A1

TITLE: Subtilisin variants

PUBLICATION-DATE: October 14, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Ness, Jon E.	Sunnyvale	CA	US	
Welch, Mark	Fremont	CA	US	
Giver, Lorraine J.	Santa Clara	CA	US	
Cherry, Joel R.	Davis	CA	US	
Borchert, Torben V.	Birkeroed	CA	DK	
Minshull, Jeremy	Menlo Park		US	

APPL-NO: 10/ 736997

DATE FILED: December 15, 2003

RELATED-US-APPL-DATA:

child 10736997 A1 20031215

parent continuation-of 09824893 20010402 US PENDING

non-provisional-of-provisional 60194143 20000403 US

US-CL-CURRENT: 435/226, 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

New subtilisin homologues (both nucleic acids and proteins) are provided. Compositions which include these new proteins, recombinant cells, shuffling methods involving the new homologues, antibodies to the new homologues, and methods of using the homologues are also provided.

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. application Ser. No. 09/824,893 filed Apr. 2, 2001, which claims priority or the benefit of U.S. Provisional Application No. 60/194,143 filed Apr. 3, 2000, the disclosure of which is incorporated herein in its entirety for all purposes.

---------- KWIC ---------

Detail Description Paragraph - DETX (35):

[0062] The polynucleotide sequences of the present invention can be engineered in order to alter a subtilisin homologue coding sequence for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, alterations may be introduced using techniques that are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, alter glycosylation patterns, change codon preference, introduce splice sites, etc.

PGPUB-DOCUMENT-NUMBER: 20040199939

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040199939 A1

TITLE: Modified cry3a toxins and nucleic acid sequences coding therefor

PUBLICATION-DATE: October 7, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Chen, Eric	Chapel Hill	NC	US	
Stacy, Cheryl	Raleigh	NC	US	

APPL-NO: 10/ 487846

DATE FILED: February 25, 2004

FOREIGN-APPL-PRIORITY-DATA:

COUNTRY	APPL-NO	DOC-ID	APPL-DATE
US	60316421	2001US-60316421	August 31, 2001

PCT-DATA:
APPL-NO: PCT/EP02/09789
DATE-FILED: Feb 9, 2002
PUB-NO:
PUB-DATE:
371-DATE:
102(E)-DATE:

US-CL-CURRENT: 800/279, 435/419 , 435/468 , 536/23.7

ABSTRACT:

Compositions and methods for controlling plant pests are disclosed. In particular, novel nucleic acid sequences encoding modified Cry3A toxins having increased toxicity to corn rootworm are provided. By inserting a protease recognition site such as cathepsin G, that is recognized by a gut protease of a target insect in at least one position of a Cry3A toxin a modified Cry3A toxin having significantly greater toxicity, particularly to western and northern corn rootworm is designed. Further, a method of making the modified Cry3A toxins and methods of using the modified Cry3A nucleic acid sequences, for example in microorganisms to control insects or in transgenic plants to confer protection from insect damage, and a method of using the modified Cry3A toxins, and compositions and formulations comprising the modified Cry3A toxins, for example applying the modified Cry3A toxins or compositions or formulations to insect-infested areas, or to prophylactically treat insect-susceptible areas or plants to confer protection against the insect pests are disclosed.

---------- KWIC ---------

Summary of Invention Paragraph - BSTX (137):
[0137] In a particularly preferred embodiment, at least one of the insecticidal modified Cry3A toxins of the invention is expressed in a higher

organism, e.g., a plant. In this case, transgenic plants expressing effective amounts of the modified Cry3A toxins protect themselves from insect pests. When the insect starts feeding on such a transgenic plant, it also ingests the expressed modified Cry3A toxins. This will deter the insect from further biting into the plant tissue or may even harm or kill the insect. A nucleotide sequence of the present invention is inserted into an expression cassette, which is then preferably stably integrated in the genome of said plant. In another preferred embodiment, the nucleotide sequence is included in a non-pathogenic self-replicating virus. Plants transformed in accordance with the present invention may be monocots or dicots and include, but are not limited to, maize, wheat, barley, rye, sweet potato, bean, pea, chicory, lettuce, cabbage, cauliflower, broccoli, turnip, radish, spinach, asparagus, onion, garlic, pepper, celery, squash, pumpkin, hemp, zucchini, apple, pear, quince, melon, plum, cherry, peach, nectarine, apricot, strawberry, grape, raspberry, blackberry, pineapple, avocado, papaya, mango, banana, soybean, tomato, sorghum, sugarcane, sugar beet, sunflower, rapeseed, clover, tobacco, carrot, cotton, alfalfa, rice, potato, eggplant, cucumber, Arabidopsis, and woody plants such as coniferous and deciduous trees. Once a desired nucleotide sequence has been transformed into a particular plant species, it may be propagated in that species or moved into other varieties of the same species, particularly including commercial varieties, using traditional breeding techniques. A nucleotide sequence of this invention is preferably expressed in transgenic plants, thus causing the biosynthesis of the corresponding modified Cry3A toxin in the transgenic plants. In this way, transgenic plants with enhanced resistance to insects are generated. For their expression in transgenic plants, the nucleotide sequences of the invention may require other modifications and optimization. Although in many cases genes from microbial organisms can be expressed in plants at high levels without modification, low expression in transgenic plants may result from microbial nucleotide sequences having codons that are not preferred in plants. It is known in the art that all organisms have specific preferences for codon usage, and the codons of the nucleotide sequences described in this invention can be changed to conform with plant preferences, while maintaining the amino acids encoded thereby. Furthermore, high expression in plants is best achieved from coding sequences that have at least about 35% GC content, preferably more than about 45%, more preferably more than about 50%, and most preferably more than about 60%. Microbial nucleotide sequences that have low GC contents may express poorly in plants due to the existence of ATTTA motifs that may destabilize messages, and AATAAA motifs that may cause inappropriate polyadenylation. Although preferred gene sequences may be adequately expressed in both monocotyledonous and dicotyledonous plant species, sequences can be modified to account for the specific codon preferences and GC content preferences of monocotyledons or dicotyledons as these preferences have been shown to differ (Murray et al. Nucl. Acids Res. 17:477-498 (1989)). In addition, the nucleotide sequences are screened for the existence of illegitimate splice sites that may cause message truncation. All changes required to be made within the nucleotide sequences such as those described above are made using well known techniques of site directed mutagenesis, PCR, and synthetic gene construction using the methods described in the published patent applications EP 0 385 962 (to Monsanto), EP 0 359 472 (to Lubrizol, and WO 93/07278 (to Ciba-Geigy).

PGPUB-DOCUMENT-NUMBER: 20040197866

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040197866 A1

TITLE: Dual expression vector system for antibody expression in bacterial and mammalian cells

PUBLICATION-DATE: October 7, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Johnson, Leslie Sydnor	Darnestown	MD	US	
Huang, Ling	Gaithersburg	MD	US	

APPL-NO: 10/ 753309

DATE FILED: January 8, 2004

RELATED-US-APPL-DATA:

non-provisional-of-provisional 60439492 20030109 US

US-CL-CURRENT: 435/69.1, 435/320.1 , 435/326 , 530/387.1 , 536/23.53

ABSTRACT:

The present invention provides a dual expression vector, and methods for its use, for the expression and secretion of a full-length polypeptide of interest in eukaryotic cells, and a soluble domain or fragment of the polypeptide in bacteria. When expressed in bacteria, transcription from a bacterial promoter within a first intron and termination at the stop codon in a second intron results in expression of a fragment of the polypeptide, e.g., a Fab fragment, whereas in mammalian cells, splicing removes the bacterial regulatory sequences located in the two introns and generates the mammalian signal sequence, allowing expression of the full-length polypeptide, e.g., IgG heavy or light chain polypeptide. The dual expression vector system of the invention can be used to select and screen for new monoclonal antibodies, as well as to optimize monoclonal antibodies for binding to antigenic molecules of interest.

[0001] This application claims the benefit of priority under 35 U.S.C. .sctn. 119(e) to provisional application No. 60/439,492, filed Jan. 9, 2003, which is incorporated by reference herein in its entirety.

---------- KWIC ---------

Detail Description Paragraph - DETX (60):

[0097] Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA in vitro or in vivo, and are commercially available from sources such as Stratagene (La Jolla, Calif.) and Promega Biotech (Madison, Wis.). In order to optimize expression and/or in vitro transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the cloned DNA to eliminate extra, potential

inappropriate alternative translation initiation codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5' of the start codon to enhance expression (see, e.g., Kozak, 1991, J. Biol. Chem. 266:19867). Similarly, alternative codons, encoding the same amino acid, can be substituted for coding sequences in order to enhance translation (e.g., the codon preference of the host cell can be adopted, the presence of G-C rich domains can be reduced, and the like).

PGPUB-DOCUMENT-NUMBER: 20040180335

PGPUB-FILING-TYPE: new

DOCUMENT-IDENTIFIER: US 20040180335 A1

TITLE: Novel chromosome 21 gene marker, compositions and methods using same

PUBLICATION-DATE: September 16, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	COUNTRY	RULE-47
Korenberg, Julie R.	Los Angeles	CA	US	
Yamakawa, Kazuhiro	Los Angeles	CA	US	

APPL-NO: 09/ 749273

DATE FILED: December 26, 2000

RELATED-US-APPL-DATA:

child 09749273 A1 20001226

parent continuation-of 09048887 19980326 US PATENTED

child 09048887 19980326 US

parent division-of 08337690 19941109 US PATENTED

US-CL-CURRENT: 435/6, 435/183 , 435/320.1 , 435/325 , 435/69.1 , 536/23.2

ABSTRACT:

The present invention provides isolated nucleic acids encoding human EHOC-1 protein and isolated receptor proteins encoded thereby. Further provided are vectors containing invention nucleic acids, probes that hybridize thereto, host cells transformed therewith, antisense oligonucleotides thereto and compositions containing, antibodies that specifically bind to invention polypeptides and compositions containing, as well as transgenic non-human mammals that express the invention protein.

---------- KWIC --------

Detail Description Paragraph - DETX (24):

[0037] Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA in vitro or in vivo, and are commercially available from sources such as Stratagene (La. Jolla, Calif.) and Promega Biotech (Madison, Wis.). In order to optimize expression and/or in vitro transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the clones to eliminate extra, potential inappropriate alternative translation initiation codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5' of the start codon to enhance expression. (See, for example, Kozak, J. Biol. Chem. 266:-9867 (1991)). Similarly, alternative codons, encoding the same

amino acid, can be substituted for coding sequences of the EHOC-1 polypeptide in order to enhance transcription (e.g., the codon preference of the host cell can be adopted, the presence of G-C rich domains can be reduced, and the like).

US-PAT-NO: 6858422

DOCUMENT-IDENTIFIER: US 6858422 B2

TITLE: Lipase genes

DATE-ISSUED: February 22, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Giver; Lorraine J.	Santa Clara	CA	N/A	N/A
Minshull; Jeremy	Menlo Park	CA	N/A	N/A
Vogel; Kurt	Palo Alto	CA	N/A	N/A

APPL-NO: 09/ 905666

DATE FILED: July 13, 2001

PARENT-CASE:

CROSS-REFERENCES TO RELATED APPLICATIONS

Pursuant to 35 USC .sctn.119(e), this application claims priority to and benefit of U.S. Provisional Patent Application Ser. No. 60/217,954, filed on Jul. 13, 2000, and 60/300,378, filed on Jun. 21, 2001, the disclosures of each of which is incorporated herein in their entirety for all purposes.

US-CL-CURRENT: 435/198, 435/195 , 435/196 , 435/197

ABSTRACT:

New lipase enzymes (both nucleic acids and polypeptides) are provided. Compositions which include these polypeptides, proteins, nucleic acids, recombinant cells, as well as methods involving the enzymes, antibodies to the enzymes, and methods of using the enzymes are also provided

31 Claims, 25 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 25

---------- KWIC ---------

Detailed Description Text - DETX (68):

The polynucleotide sequences of the present invention can be engineered in order to alter lipase homologue coding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, alterations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis, to insert new restriction sites, to alter glycosylation patterns or other conjugation patterns, to change codon preference, to introduce splice sites, to introduce or remove introns, etc.

US-PAT-NO: 6855316

DOCUMENT-IDENTIFIER: US 6855316 B1

TITLE: Baculovirus produced Plasmodium falciparum vaccine

DATE-ISSUED: February 15, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Chang; Sandra P.	Honolulu	HI	N/A	N/A
Kramer; Kenton J.	Kaneohe	HI	N/A	N/A
Gosnell; William L.	Honolulu	HI	N/A	N/A
Nishimura; Tani	Honolulu	HI	N/A	N/A

APPL-NO: 09/ 500376

DATE FILED: February 8, 2000

PARENT-CASE:

This application is a continuation-in-part of application Ser. No.: 08/195,705, filed Feb. 14, 1994, now U.S. Pat. No. 6,420,523.

US-CL-CURRENT: 424/185.1, 424/265.1

ABSTRACT:

Compositions and methods are provided for the induction of a protective immunize response in primates against lethal challenge of Plasmodium.

19 Claims, 39 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 21

---------- KWIC ---------

Detailed Description Text - DETX (108):
The nucleotide sequence of the original BVp42 construct was modified to optimize for insect cell line (High Five, Trichoplusia ni) codon preferences, distance between the promoter sequence and translation initiation codon, and preferred nucleotide composition of the sequences immediately before the initiation codon. The modified construct has been designated BVp42-M and the nucleotide sequence of this construct is shown in FIG. 12.

Detailed Description Text - DETX (111):
The K1 type (p42-K) of the p42 antigen was constructed using the Vietnam-Oak Knoll P. falciparum isolate (FVO). There are three parts to this construct: a leader sequence, the p42-K coding region and the histidine tag (FIG. 13). Restriction sites were incorporated into the primers to enable a "sticky-end" ligation of the three fragments. The leader sequence was altered from the original p42-M sequence such that three adenines were added three bases prior to the start site to optimize the codon preference for baculovirus and insect cells as well as the distance between the promoter sequence and the methionine

start codon (Ranjan et al 1995. Virus Genes 9(2):149-153). Primers containing NarI and PstI restriction site sequences were used to amplify the 1,065 base pair p42-K coding region corresponding to the Ala.sub.1349 to Ser.sub.1723 (as numbered by Miller et at 1993. Mol. Biochem. Parasitol 59(1):1-14.) of MSP- 1 from genomic P. falciparum DNA. Primers containing BamHI and NarI restriction site sequences were used to amplify the 91 base pair leader sequence. Oligonucleotides containing PstI and KpnI restriction site sequences were made to generate the 25 base pair histidine tag. All primers and oligonucleotide sequences used for the p42-K constructs are shown in Table 1.

US-PAT-NO: 6844431

DOCUMENT-IDENTIFIER: US 6844431 B1

TITLE: Nucleic acid encoding spinocerebellar ataxia-2 and products related thereto

DATE-ISSUED: January 18, 2005

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Pulst; Stefan M.	Los Angeles	CA	N/A	N/A

APPL-NO: 08/ 981998

DATE FILED: May 11, 1998

PARENT-CASE:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a U.S. National Stage application which claims priority to International Application No. PCT/US97/07725 (filed May 8, 1997), which is a continuation-in-part of U.S. patent application Ser. No. 08/727,084 (filed Oct. 8, 1996), now abandoned, which further claims priority to provisional application Serial No. 60/017,388 (filed May 8, 1996) and 60/022,207 (filed Jul. 19, 1996), all of which are incorporated herein by reference.

PCT-DATA:
APPL-NO: PCT/US97/07725
DATE-FILED: May 8, 1997
PUB-NO: WO97/42314
PUB-DATE: Nov 13, 1997
371-DATE: May 11, 1998
102(E)-DATE:May 11, 1998

US-CL-CURRENT: 536/23.1, 435/320.1 , 435/6 , 536/24.31 , 536/24.33

ABSTRACT:

The present invention provides isolated nucleic acids encoding human SCA2 protein, or fragments thereof, and isolated SCA2 proteins encoded thereby. Further provided are vectors containing invention nucleic acids, probes that hybridize thereto, host cells transformed therewith, antisense oligonucleotides thereto and compositions containing antibodies that specifically bind to invention polypeptides, as well as transgenic non-human mammals that express the invention protein. In addition, methods for diagnosing spinocerebellar Ataxia Type 2 are provided.

8 Claims, 14 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 14

---------- KWIC ---------

Detailed Description Text - DETX (23):

Vectors that contain both a promoter and a cloning site into which a polynucleotide can be operatively linked are well known in the art. Such vectors are capable of transcribing RNA in vitro or in vivo, and are commercially available from sources such as Stratagene (La Jolla, Calif.) and Promega Biotech (Madison, Wis.). In order to optimize expression and/or in vitro transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the clones to eliminate extra, potential inappropriate alternative translation initiation codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites can be inserted immediately 5' of the start codon to enhance expression. (See, for example, Kozak, J. Biol. Chem. 266:19867 (1991)). Similarly, alternative codons, encoding the same amino acid, can be substituted for coding sequences of the SCA2 polypeptide in order to enhance transcription (e.g., the codon preference of the host cell can be adopted, the presence of G-C rich domains can be reduced, and the like).

US-PAT-NO: 6825322

DOCUMENT-IDENTIFIER: US 6825322 B2

TITLE: Human N-methyl-D-aspartate receptor subunits, nucleic acids encoding same and uses therefor

DATE-ISSUED: November 30, 2004

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Daggett; Lorrie P.	San Diego	CA	N/A	N/A
Lu; Chin-Chun	San Diego	CA	N/A	N/A

APPL-NO: 10/ 038937

DATE FILED: January 4, 2002

PARENT-CASE:

CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a Divisional application based on Ser. No. 08/935,105, filed Sep. 29, 1997, now U.S. Pat. No. 6,376,660 which is a Divisional of Ser. No. 08/231,193, filed Apr. 20, 1994, now U.S. Pat. No. 5,849,895, which is a continuation-in-part of U.S. Ser. No. 08/052,449, filed Apr. 20, 1993, now abandoned.

US-CL-CURRENT: 530/350, 435/69.1 , 435/7.21 , 436/501 , 536/23.5

ABSTRACT:

In accordance with the present invention, there are provided nucleic acids encoding human NMDA receptor protein subunits and the proteins encoded thereby. The NMDA receptor subunits of the invention comprise components of NMDA receptors that have cation-selective channels and bind glutamate and NMDA. In one aspect of the invention, the nucleic acids encode NMDAR1 and NMDAR2 subunits of human NMDA receptors. In a preferred embodiment, the invention nucleic acids encode NMDAR1, NMDAR2A, NMDAR2B, NMDAR2C and NMDAR2D subunits of human NMDA receptors. In addition to being useful for the production of NMDA receptor subunit proteins, these nucleic acids are also useful as probes, thus enabling those skilled in the art, without undue experimentation, to identify and isolate related human receptor subunits. Functional glutamate receptors can be assembled, in accordance with the present invention, from a plurality of one type of NMDA receptor subunit protein (homomeric) or from a mixture of two or more types of subunit proteins (heteromeric). In addition to disclosing novel NMDA receptor protein subunits, the present invention also comprises methods for using such receptor subunits to identify and characterize compounds which affect the function of such receptors, e.g., agonists, antagonists, and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are functional as NMDA receptor subunits.

3 Claims, 7 Drawing figures

Exemplary Claim Number: 1

Number of Drawing Sheets: 7

---------- KWIC ---------

Detailed Description Text - DETX (48):

As used herein, the term "operatively linked" refers to the functional relationship of DNA with regulatory and effector sequences of nucleotides, such as promoters, enhancers, transcriptional and translational stop sites, and other signal sequences. For example, operative linkage of DNA to a promoter refers to the physical and functional relationship between the DNA and the promoter such that the transcription of such DNA is initiated from the promoter by an RNA polymerase that specifically recognizes and binds to the promoter, and transcribes the DNA. In order to optimize expression and/or in vitro transcription, it may be necessary to remove, add or alter 5' and/or 3' untranslated portions of the clones to eliminate extra, potential inappropriate alternative translation initiation (i.e., start) codons or other sequences that may interfere with or reduce expression, either at the level of transcription or translation. Alternatively, consensus ribosome binding sites (see, for example, Kozak (1991) J. Biol. Chem. 266:19867-19870) can be inserted immediately 5' of the start codon and may enhance expression. Likewise, alternative codons, encoding the same amino acid, can be substituted for coding sequences of the NMDAR subunits in order to enhance transcription (e.g., the codon preference of the host cells can be adopted, the presence of G-C rich domains can be reduced, and the like). Furthermore, for potentially enhanced expression of NMDA receptor subunits in amphibian oocytes, the subunit coding sequence can optionally be incorporated into an expression construct wherein the 5'- and 3'-ends of the coding sequence are contiguous with Xenopus .beta.-globin gene 5' and 3' untranslated sequences, respectively. For example, NMDA receptor subunit coding sequences can be incorporated into vector pSP64T (see Krieg and Melton (1984) in Nucleic Acids Research 12:7057-7070), a modified form of pSP64 (available from Promega, Madison, Wis.). The coding sequence is inserted between the 5' end of the .beta.-globin gene and the 3' untranslated sequences located downstream of the SP6 promoter. In vitro transcripts can then be generated from the resulting vector. The desirability of (or need for) such modification may be empirically determined.

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  * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 15:26:29 ON 07 MAR 2005

=> fil .bec
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                        17.53      18.01

FILES 'MEDLINE, SCISEARCH, LIFESCI, BIOTECHDS, BIOSIS, EMBASE, HCAPLUS, NTIS,
       ESBIOBASE, BIOTECHNO, WPIDS' ENTERED AT 15:30:31 ON 07 MAR 2005
ALL COPYRIGHTS AND RESTRICTIONS APPLY.  SEE HELP USAGETERMS FOR DETAILS.

11 FILES IN THE FILE LIST

=> s (synthetic or variant or modif? or alter?)(5a)(gene/q or nucleic acid#)
FILE 'MEDLINE'
        125368 SYNTHETIC
         61082 VARIANT
        374047 MODIF?
        654982 ALTER?
        173777 NUCLEIC
       1521135 ACID#
        173387 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L1       43075 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'SCISEARCH'
        156969 SYNTHETIC
         65585 VARIANT
        496937 MODIF?
        652720 ALTER?
         33410 NUCLEIC
       1220427 ACID#
         32937 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L2       43087 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'LIFESCI'
         39060 SYNTHETIC
         18202 VARIANT
         94176 MODIF?
        176125 ALTER?
         12771 "NUCLEIC"
        317175 ACID#
         12609 NUCLEIC ACID#
                 ("NUCLEIC"(W)ACID#)
L3       21722 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'BIOTECHDS'
         13081 SYNTHETIC
          9107 VARIANT
         33901 MODIF?
         26353 ALTER?
         41771 NUCLEIC
        135130 ACID#
         41690 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L4       15267 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)
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FILE 'BIOSIS'
        194099 SYNTHETIC
         61573 VARIANT
        370717 MODIF?
        655940 ALTER?
         50317 NUCLEIC
       1328897 ACID#
         49729 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L5       47899 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'EMBASE'
        106824 SYNTHETIC
         56726 VARIANT
        334698 MODIF?
        614957 ALTER?
         34184 "NUCLEIC"
       1328817 ACID#
         33897 NUCLEIC ACID#
                 ("NUCLEIC"(W)ACID#)
L6       39584 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'HCAPLUS'
        557045 SYNTHETIC
         57102 VARIANT
        904538 MODIF?
        828063 ALTER?
        166429 NUCLEIC
       4423278 ACID#
        165464 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L7       70134 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'NTIS'
         18802 SYNTHETIC
          2539 VARIANT
         96549 MODIF?
         90587 ALTER?
          1806 NUCLEIC
         54530 ACID#
          1790 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L8         960 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'ESBIOBASE'
         39482 SYNTHETIC
         23902 VARIANT
        142863 MODIF?
        231481 ALTER?
         24367 NUCLEIC
        357503 ACID#
         24251 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L9       23973 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'BIOTECHNO'
         41250 SYNTHETIC
         25068 VARIANT
         86734 MODIF?
```

```
        148127 ALTER?
         19939 NUCLEIC
        371908 ACID#
         19837 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L10      27490 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

FILE 'WPIDS'
        214971 SYNTHETIC
         18390 VARIANT
        265508 MODIF?
        427717 ALTER?
         53292 NUCLEIC
        923785 ACID#
         53034 NUCLEIC ACID#
                 (NUCLEIC(W)ACID#)
L11      17641 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

TOTAL FOR ALL FILES
L12     350832 (SYNTHETIC OR VARIANT OR MODIF? OR ALTER?)(5A)(GENE/Q OR NUCLEIC
               ACID#)

=> s codon(3a)(choice# or preference# or select?)
FILE 'MEDLINE'
         34716 CODON
        125141 CHOICE#
         45905 PREFERENCE#
        656383 SELECT?
L13        452 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'SCISEARCH'
         24833 CODON
        120699 CHOICE#
         61641 PREFERENCE#
        840750 SELECT?
L14        451 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'LIFESCI'
         14179 CODON
         20096 CHOICE#
         28344 PREFERENCE#
        208181 SELECT?
L15        324 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'BIOTECHDS'
          5137 CODON
          1483 CHOICE#
           854 PREFERENCE#
         63779 SELECT?
L16        125 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'BIOSIS'
         28514 CODON
         76564 CHOICE#
         60873 PREFERENCE#
        700743 SELECT?
L17        490 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'EMBASE'
         27696 CODON
        110245 CHOICE#
         38854 PREFERENCE#
```

```
        600364 SELECT?
L18        393 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'HCAPLUS'
         34079 CODON
         82697 CHOICE#
         41632 PREFERENCE#
       1154859 SELECT?
L19        689 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'NTIS'
            92 CODON
         19309 CHOICE#
          4870 PREFERENCE#
        163997 SELECT?
L20           2 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'ESBIOBASE'
         14210 CODON
         32606 CHOICE#
         19501 PREFERENCE#
        260193 SELECT?
L21        259 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'BIOTECHNO'
         21971 CODON
          8409 CHOICE#
          7785 PREFERENCE#
        148138 SELECT?
L22        314 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

FILE 'WPIDS'
          2691 CODON
         27054 CHOICE#
          6765 PREFERENCE#
       1026281 SELECT?
L23         87 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

TOTAL FOR ALL FILES
L24       3586 CODON(3A)(CHOICE# OR PREFERENCE# OR SELECT?)

=> s l12 and l24
FILE 'MEDLINE'
L25         39 L1 AND L13

FILE 'SCISEARCH'
L26         26 L2 AND L14

FILE 'LIFESCI'
L27         18 L3 AND L15

FILE 'BIOTECHDS'
L28         38 L4 AND L16

FILE 'BIOSIS'
L29         32 L5 AND L17

FILE 'EMBASE'
L30         26 L6 AND L18

FILE 'HCAPLUS'
L31         81 L7 AND L19

FILE 'NTIS'
```

```
L32           0 L8 AND L20

FILE 'ESBIOBASE'
L33          17 L9 AND L21

FILE 'BIOTECHNO'
L34          20 L10 AND L22

FILE 'WPIDS'
L35          27 L11 AND L23

TOTAL FOR ALL FILES
L36         324 L12 AND L24

=> s l36 not 2001-2005/py
FILE 'MEDLINE'
       2295382 2001-2005/PY
L37          30 L25 NOT 2001-2005/PY

FILE 'SCISEARCH'
       4252440 2001-2005/PY
L38          19 L26 NOT 2001-2005/PY

FILE 'LIFESCI'
        404734 2001-2005/PY
L39          16 L27 NOT 2001-2005/PY

FILE 'BIOTECHDS'
         93501 2001-2005/PY
L40          14 L28 NOT 2001-2005/PY

FILE 'BIOSIS'
       2086835 2001-2005/PY
L41          28 L29 NOT 2001-2005/PY

FILE 'EMBASE'
       1971331 2001-2005/PY
L42          21 L30 NOT 2001-2005/PY

FILE 'HCAPLUS'
       4333866 2001-2005/PY
L43          48 L31 NOT 2001-2005/PY

FILE 'NTIS'
         60375 2001-2005/PY
L44           0 L32 NOT 2001-2005/PY

FILE 'ESBIOBASE'
       1206077 2001-2005/PY
L45          12 L33 NOT 2001-2005/PY

FILE 'BIOTECHNO'
        368875 2001-2005/PY
L46          19 L34 NOT 2001-2005/PY

FILE 'WPIDS'
       3922086 2001-2005/PY
L47           3 L35 NOT 2001-2005/PY

TOTAL FOR ALL FILES
L48         210 L36 NOT 2001-2005/PY

=> s (transcription factor# or splice or poly(w)'a' or polyadenylat? or
promoter)(5a)(site# or sequence#)(15a)(reduc? or lower? or decreas?)
```

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FILE 'MEDLINE'
        241660 TRANSCRIPTION
       2237838 FACTOR#
        101781 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
         12924 SPLICE
         56851 POLY
       8074978 'A'
          6836 POLYADENYLAT?
        107079 PROMOTER
        678528 SITE#
        733840 SEQUENCE#
       1174513 REDUC?
        659256 LOWER?
        940503 DECREAS?
L49       1023 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'SCISEARCH'
        190948 TRANSCRIPTION
       1330426 FACTOR#
         73764 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
         14239 SPLICE
        161759 POLY
      10063027 'A'
          5395 POLYADENYLAT?
        108327 PROMOTER
        720454 SITE#
        591268 SEQUENCE#
       1335369 REDUC?
        751820 LOWER?
        938069 DECREAS?
L50       1291 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'LIFESCI'
         98844 "TRANSCRIPTION"
        297592 FACTOR#
         34957 TRANSCRIPTION FACTOR#
                 ("TRANSCRIPTION"(W)FACTOR#)
          6502 SPLICE
         17479 POLY
       2071889 'A'
          4201 POLYADENYLAT?
         58090 PROMOTER
        263528 SITE#
        265607 SEQUENCE#
        290200 REDUC?
        142417 LOWER?
        221982 DECREAS?
L51        921 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'BIOTECHDS'
         15896 TRANSCRIPTION
         36977 FACTOR#
          2136 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
          1352 SPLICE
          6826 POLY
```

```
        339262 'A'
          1632 POLYADENYLAT?
         32187 PROMOTER
         35949 SITE#
        106231 SEQUENCE#
         47812 REDUC?
         17334 LOWER?
         23037 DECREAS?
L52        189 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'BIOSIS'
        213000 TRANSCRIPTION
       1240455 FACTOR#
         64856 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
         13712 SPLICE
        140609 POLY
       7888132 'A'
          7622 POLYADENYLAT?
        115348 PROMOTER
        693282 SITE#
        532953 SEQUENCE#
       1213058 REDUC?
        722398 LOWER?
       1050263 DECREAS?
L53       1024 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'EMBASE'
        224682 "TRANSCRIPTION"
       1162109 FACTOR#
         65898 TRANSCRIPTION FACTOR#
                 ("TRANSCRIPTION"(W)FACTOR#)
         11449 SPLICE
         49216 POLY
       6994633 'A'
          7036 POLYADENYLAT?
         91945 PROMOTER
        562660 SITE#
        520538 SEQUENCE#
       1108862 REDUC?
        610737 LOWER?
        883001 DECREAS?
L54        1358 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

FILE 'HCAPLUS'
        273392 TRANSCRIPTION
       1412747 FACTOR#
        130412 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
         16128 SPLICE
        631162 POLY
      18625074 'A'
         10980 POLYADENYLAT?
        156915 PROMOTER
        879380 SITE#
        755047 SEQUENCE#
       1915982 REDUC?
        842240 REDN
```

```
        2378515 REDUC?
                  (REDUC? OR REDN)
        1336543 LOWER?
        2145283 DECREAS?
L55        1473 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
                OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
                DECREAS?)

FILE 'NTIS'
           1788 TRANSCRIPTION
         147502 FACTOR#
            404 TRANSCRIPTION FACTOR#
                  (TRANSCRIPTION(W)FACTOR#)
            468 SPLICE
           5585 POLY
        1660107 'A'
             12 POLYADENYLAT?
            961 PROMOTER
         122342 SITE#
          28403 SEQUENCE#
         178866 REDUC?
          67037 LOWER?
          51462 DECREAS?
L56            0 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
                OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
                DECREAS?)

FILE 'ESBIOBASE'
         109278 TRANSCRIPTION
         424227 FACTOR#
          48010 TRANSCRIPTION FACTOR#
                  (TRANSCRIPTION(W)FACTOR#)
           8322 SPLICE
          16901 POLY
        2261678 'A'
           2675 POLYADENYLAT?
          58030 PROMOTER
         443485 SITE#
         238803 SEQUENCE#
         414704 REDUC?
         227403 LOWER?
         329135 DECREAS?
L57         983 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
                OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
                DECREAS?)

FILE 'BIOTECHNO'
         160885 TRANSCRIPTION
         296524 FACTOR#
          41412 TRANSCRIPTION FACTOR#
                  (TRANSCRIPTION(W)FACTOR#)
           8894 SPLICE
          21682 POLY
        1454372 'A'
           5860 POLYADENYLAT?
          72959 PROMOTER
         222731 SITE#
         375038 SEQUENCE#
         232937 REDUC?
         106436 LOWER?
         171676 DECREAS?
L58        1101 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
                OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
                DECREAS?)
```

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FILE 'WPIDS'
         12993 TRANSCRIPTION
        155288 FACTOR#
          2068 TRANSCRIPTION FACTOR#
                 (TRANSCRIPTION(W)FACTOR#)
          9799 SPLICE
        158200 POLY
       1853461 'A'
           918 POLYADENYLAT?
         32236 PROMOTER
        120688 SITE#
        243707 SEQUENCE#
       2069811 REDUC?
         61105 REDN
       2095227 REDUC?
                 (REDUC? OR REDN)
       1175467 LOWER?
        214255 DECREAS?
L59        144 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W)'A' OR POLYADENYLAT?
               OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

TOTAL FOR ALL FILES
L60       9507 (TRANSCRIPTION FACTOR# OR SPLICE OR POLY(W) 'A' OR POLYADENYLAT?
                OR PROMOTER)(5A)(SITE# OR SEQUENCE#)(15A)(REDUC? OR LOWER? OR
               DECREAS?)

=> s l12 and l60
FILE 'MEDLINE'
L61          75 L1 AND L49

FILE 'SCISEARCH'
L62          70 L2 AND L50

FILE 'LIFESCI'
L63          53 L3 AND L51

FILE 'BIOTECHDS'
L64          43 L4 AND L52

FILE 'BIOSIS'
L65          71 L5 AND L53

FILE 'EMBASE'
L66          81 L6 AND L54

FILE 'HCAPLUS'
L67         151 L7 AND L55

FILE 'NTIS'
L68           0 L8 AND L56

FILE 'ESBIOBASE'
L69          51 L9 AND L57

FILE 'BIOTECHNO'
L70          67 L10 AND L58

FILE 'WPIDS'
L71          50 L11 AND L59

TOTAL FOR ALL FILES
L72         712 L12 AND L60
```

```
=> s l24 and l60
FILE 'MEDLINE'
L73             0 L13 AND L49

FILE 'SCISEARCH'
L74             0 L14 AND L50

FILE 'LIFESCI'
L75             0 L15 AND L51

FILE 'BIOTECHDS'
L76             0 L16 AND L52

FILE 'BIOSIS'
L77             0 L17 AND L53

FILE 'EMBASE'
L78             0 L18 AND L54

FILE 'HCAPLUS'
L79             1 L19 AND L55

FILE 'NTIS'
L80             0 L20 AND L56

FILE 'ESBIOBASE'
L81             0 L21 AND L57

FILE 'BIOTECHNO'
L82             0 L22 AND L58

FILE 'WPIDS'
L83             0 L23 AND L59

TOTAL FOR ALL FILES
L84             1 L24 AND L60

=> s l12(15a)l60
FILE 'MEDLINE'
L85            14 L1 (15A)L49

FILE 'SCISEARCH'
L86            15 L2 (15A)L50

FILE 'LIFESCI'
L87            13 L3 (15A)L51

FILE 'BIOTECHDS'
L88            11 L4 (15A)L52

FILE 'BIOSIS'
L89            11 L5 (15A)L53

FILE 'EMBASE'
L90            21 L6 (15A)L54

FILE 'HCAPLUS'
L91            49 L7 (15A)L55

FILE 'NTIS'
L92             0 L8 (15A)L56

FILE 'ESBIOBASE'
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L93          12 L9 (15A)L57

FILE 'BIOTECHNO'
L94          14 L10(15A)L58

FILE 'WPIDS'
L95          20 L11(15A)L59

TOTAL FOR ALL FILES
L96         180 L12(15A) L60


=> s (184 or 196) not 2001-2005/py
FILE 'MEDLINE'
       2295382 2001-2005/PY
L97          11 (L73 OR L85) NOT 2001-2005/PY

FILE 'SCISEARCH'
       4252440 2001-2005/PY
L98          11 (L74 OR L86) NOT 2001-2005/PY

FILE 'LIFESCI'
        404734 2001-2005/PY
L99          12 (L75 OR L87) NOT 2001-2005/PY

FILE 'BIOTECHDS'
         93501 2001-2005/PY
L100          4 (L76 OR L88) NOT 2001-2005/PY

FILE 'BIOSIS'
       2086835 2001-2005/PY
L101          9 (L77 OR L89) NOT 2001-2005/PY

FILE 'EMBASE'
       1971331 2001-2005/PY
L102         16 (L78 OR L90) NOT 2001-2005/PY

FILE 'HCAPLUS'
       4333866 2001-2005/PY
L103         20 (L79 OR L91) NOT 2001-2005/PY

FILE 'NTIS'
         60375 2001-2005/PY
L104          0 (L80 OR L92) NOT 2001-2005/PY

FILE 'ESBIOBASE'
       1206077 2001-2005/PY
L105          8 (L81 OR L93) NOT 2001-2005/PY

FILE 'BIOTECHNO'
        368875 2001-2005/PY
L106         14 (L82 OR L94) NOT 2001-2005/PY

FILE 'WPIDS'
       3922086 2001-2005/PY
L107          3 (L83 OR L95) NOT 2001-2005/PY

TOTAL FOR ALL FILES
L108        108 (L84 OR L96) NOT 2001-2005/PY

=> log y
COST IN U.S. DOLLARS                        SINCE FILE      TOTAL
                                              ENTRY    SESSION
FULL ESTIMATED COST                           72.97      90.98
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STN INTERNATIONAL LOGOFF AT 15:51:47 ON 07 MAR 2005